c1129	12	2.2	15	1	AAT52130	Human ICAM hammerh
1130	12	2.2	15	1	AAT46990	HLA sequence 29.
c1131	12	2.2	15	1	AAV57003	Human Notch3 gene
c1132	12	2.2	15	1	AAX28221	Tumour antigen ant
c1133	12	2.2	15	1	AAZ90118	PCR primer H-T11A
1134	12	2.2	15	1	AAI67276	Human FKBP8 allele
c1135	12	2.2	15	1	AAI71747	PCR primer #2. Sy
c1136	12	2.2	15	1	AAH55207	Genomic DNA methyl
1137	12	2.2	15	1	AAH55208	Genomic DNA methyl
c1138	12	2.2	15	1	AAH55211	Genomic DNA methyl
1139	12	2.2	15	1	AAH55212	Genomic DNA methyl
c1140	12	2.2	15	1	AAH23587	Dye-labeled dideox
c1141	12	2.2	15	1	AAF81549	Dye-labeled molecu
1142	12	2.2	15	1	AAF48795	IGFBP3 oligonucleo
1143	12	2.2	15	1	AAF48796	IGFBP3 oligonucleo
c1144	12	2.2	15	1	AAF53599	IGF-I oligonucleot
c1145	12	2.2	15	1	AAF53600	IGF-I oligonucleot
c1146	12	2.2	15	1	AAF53601	IGF-I oligonucleot
c1147	12	2.2	15	1	AAF53602	IGF-I oligonucleot
c1148	12	2.2	15	1	ABS64182	Tachykinin recepto
c1149	12	2.2	15	1	ABK72343	Human HTR5A gene a
1150	12	2.2	15	1	ABK54455	ASO primer #5 to d
1151	12	2.2	15	1	AAD26754	Human SNAP29 gene
1152	12	2.2	15	1	AAD26043	Human apolipoprote
c1153	12	2.2	15	1	AAD26058	Human apolipoprote
1154	12	2.2	15	1	ABI99093	Human PCDH2 ASO PC

ALIGNMENTS

RESULT 1
ABZ00175
ID ABZ00175 standard; DNA; 50 BP.
XX
AC ABZ00175;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 166.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection;
KW probe; ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US47856.
XX
PR 20-OCT-2000; 2000US-241994P.
PR 08-JUN-2001; 2001US-296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quertermous T, Johnson F;
XX
DR WPI; 2002-636525/68.
XX
PT New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides -
XX
PS Claim 1; Page 332; 2038pp; English.
XX
CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection.
XX
SQ Sequence 50 BP; 11 A; 18 C; 6 G; 15 T; 0 other;

Query Match 9.3%; Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1385 GCCTTCATGCACCTGTCCTTTCTAACACGTCGCCTTCAACTGTAATCACA 1434
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GCCTTCATGCACCTGTCCTTTCTAACACGTCGCCTTCAACTGTAATCACA 50

RESULT 2
ABZ04679
ID ABZ04679 standard; DNA; 50 BP.
XX
AC ABZ04679;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 4670.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection;
KW probe; ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US47856.
XX
PR 20-OCT-2000; 2000US-241994P.
PR 08-JUN-2001; 2001US-296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quertermous T, Johnson F;
XX
DR WPI; 2002-636525/68.
XX
PT New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides -
XX
PS Claim 1; Page 477; 2038pp; English.
XX
CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection.
XX

ATTACHMENT

APPLICANT'S IDS [illegible]
COPY

```
SQ   Sequence 50 BP; 13 A; 17 C; 5 G; 15 T; 0 other;

  Query Match             9.3%;  Score 50;  DB 1;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 0.00018;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1404 TTCTAACACGTCGCCTTCAACTGTAATCACAACATCCTGACTCCGTCATT 1453
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTAACACGTCGCCTTCAACTGTAATCACAACATCCTGACTCCGTCATT 50


RESULT 3
AAH88905
ID   AAH88905 standard; DNA; 21 BP.
XX
AC   AAH88905;
XX
DT   27-FEB-2002  (first entry)
XX
DE   Human polymorphic oligonucleotide AC003693 fragment #1.
XX
KW   Human; single nucleotide polymorphic; SNP; forensic science;
KW   paternity testing; phenotypic trait; genetic mapping; animal breeding;
KW   plant breeding; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,g)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200134840-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-US30766.
XX
PR   10-NOV-1999;   99US-0164596.
XX
PA   (GLAX ) GLAXO GROUP LTD.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Au K,  Chen J,  Patil N,  Thomas D;
XX
DR   WPI; 2001-335945/35.
XX
PT   New polymorphic sites derived from the human genome are useful to
PT   determine sites correlating with phenotypic traits, particularly
PT   disease, and also in forensics and paternity testing  -
XX
PS   Claim 37; Page 9; 43pp; English.
XX
CC   The present invention relates to human oligonucleotides comprising a
CC   single nucleotide polymorphic site (SNP: AAH88797-AAH89219). The present
CC   sequence is one such oligonucleotide. The oligonucleotides can be used in
CC   forensics, paternity testing, correlation of polymorphisms with
CC   phenotypic traits, genetic mapping of phenotypic traits and marker
CC   assisted breeding of animals and crop plants.
XX
SQ   Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 other;

  Query Match             3.9%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        979 TGCAGTGCCCCCTAAGTGACC 999
              |||||||||||||||||||||
Db          1 TGCAGTGCCCCCTAAGTGACC 21


RESULT 4
AAH88906
ID   AAH88906 standard; DNA; 21 BP.
XX
AC   AAH88906;
XX
DT   27-FEB-2002  (first entry)
XX
DE   Human polymorphic oligonucleotide AC003693 fragment #2.
XX
KW   Human; single nucleotide polymorphic; SNP; forensic science;
KW   paternity testing; phenotypic trait; genetic mapping; animal breeding;
KW   plant breeding; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,t)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200134840-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-US30766.
XX
PR   10-NOV-1999;   99US-0164596.
XX
PA   (GLAX ) GLAXO GROUP LTD.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Au K,  Chen J,  Patil N,  Thomas D;
XX
DR   WPI; 2001-335945/35.
XX
PT   New polymorphic sites derived from the human genome are useful to
PT   determine sites correlating with phenotypic traits, particularly
PT   disease, and also in forensics and paternity testing  -
XX
PS   Claim 37; Page 9; 43pp; English.
XX
CC   The present invention relates to human oligonucleotides comprising a
CC   single nucleotide polymorphic site (SNP: AAH88797-AAH89219). The present
CC   sequence is one such oligonucleotide. The oligonucleotides can be used in
CC   forensics, paternity testing, correlation of polymorphisms with
CC   phenotypic traits, genetic mapping of phenotypic traits and marker
CC   assisted breeding of animals and crop plants.
XX
SQ   Sequence 21 BP; 5 A; 5 C; 3 G; 8 T; 0 other;

  Query Match             3.9%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1036 ATAACGTTTCCGGTATTACTC 1056
              |||||||||||||||||||||
Db          1 ATAACGTTTCCGGTATTACTC 21


RESULT 5
AAC96345/c
ID   AAC96345 standard; DNA; 25 BP.
XX
AC   AAC96345;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #77.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
```

```
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP03636.
XX
PR   26-APR-1999;   99EP-0303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences
PT   of specific length  -
XX
PS   Claim 14; Page 49; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular.
XX
SQ   Sequence 25 BP; 2 A; 5 C; 3 G; 15 T; 0 other;

  Query Match             3.8%;  Score 20.4;  DB 1;  Length 25;
  Best Local Similarity   95.5%;  Pred. No. 66;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1471 CAGGCATGCTAAAAAAAAAAA 1492
             |||| ||||||||||||||||||
Db         22 CAGGAATGCTAAAAAAAAAAA 1

RESULT 6
AAQ75716/c
ID   AAQ75716 standard; DNA; 21 BP.
XX
AC   AAQ75716;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;

  Query Match             3.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1477 TGCTAAAAAAAAAAAAAAAA 1496
             ||||||||||||||||||||
Db         21 TGCTAAAAAAAAAAAAAAAA 2

RESULT 7
AAQ75661/c
ID   AAQ75661 standard; DNA; 21 BP.
XX
AC   AAQ75661;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;

  Query Match             3.6%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 63;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1476 ATGCTAAAAAAAAAAAAAAA 1496
             |||| ||||||||||||||||||
Db         21 ATGCAAAAAAAAAAAAAAAA 1
```

```
RESULT 8
AAQ49436/c
ID   AAQ49436 standard; cDNA; 20 BP.
XX
AC   AAQ49436;
XX
DT   25-MAR-2003  (updated)
DT   27-APR-1994  (first entry)
XX
DE   Cytochrome P450 sequence amplification PCR primer polyT.
XX
KW   Transgenic plants; altered petal colour;
KW   polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9320206-A1.
XX
PD   14-OCT-1993.
XX
PF   25-MAR-1993;   93WO-AU00127.
XX
PR   27-MAR-1992;   92AU-0001538.
PR   07-JAN-1993;   93AU-0006698.
XX
PA   (ITFL-) INT FLOWER DEV PTY LTD.
XX
PI   Cornish EC,  Holton TA,  Tanaka Y;
XX
DR   WPI; 1993-336914/42.
XX
PT   Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to
PT   create transgenic plants with altered petal colour
XX
PS   Disclosure; Page 25; 86pp; English.
XX
CC   The sequence is that of a PCR primer which was used in polymerase
CC   chain reactions for the amplification of cloned cytochrome P450
CC   sequences.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;

  Query Match             3.5%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1478 GCTAAAAAAAAAAAAAAAA 1496
              ||||||||||||||||||
Db         20 GCTAAAAAAAAAAAAAAAA 2


RESULT 9
AAQ75578/c
ID   AAQ75578 standard; DNA; 20 BP.
XX
AC   AAQ75578;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;

  Query Match             3.5%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1478 GCTAAAAAAAAAAAAAAAA 1496
              ||||||||||||||||||
Db         20 GCTAAAAAAAAAAAAAAAA 2


RESULT 10
AAQ75715/c
ID   AAQ75715 standard; DNA; 21 BP.
XX
AC   AAQ75715;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
```